

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/562,081
Source: IFWP
Date Processed by STIC: 01/09/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)**
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/562,081

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWP

RAW SEQUENCE LISTING

DATE: 01/09/2006

PATENT APPLICATION: US/10/562,081

TIME: 11:14:15

Input Set : A:\50318.011001.ST25.txt

Output Set: N:\CRF4\01092006\J562081.raw

3 <110> APPLICANT: Vuolteenaho, Olli
 4 Ala-Kopsala, Minna
 5 Ruskoaho, Heikki
 6 Leppaluoto, Juhani
 7 Haapalahti, Jouko
 9 <120> TITLE OF INVENTION: Assay
 11 <130> FILE REFERENCE: 50318/011001
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/562,081
 C--> 13 <141> CURRENT FILING DATE: 2005-12-23
 13 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/006971
 14 <151> PRIOR FILING DATE: 2004-06-28
 16 <150> PRIOR APPLICATION NUMBER: GB 031 5291.5
 17 <151> PRIOR FILING DATE: 2003-06-30
 19 <160> NUMBER OF SEQ ID NOS: 36
 21 <170> SOFTWARE: PatentIn version 3.3
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 126
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Homo sapiens
 28 <400> SEQUENCE: 1
 30 Asn Pro Met Tyr Asn Ala Val Ser Asn Ala Asp Leu Met Asp Phe Lys
 31 1 5 10 15
 34 Asn Leu Leu Asp His Leu Glu Glu Lys Met Pro Leu Glu Asp Glu Val
 35 20 25 30
 38 Val Pro Pro Gln Val Leu Ser Glu Pro Asn Glu Glu Ala Gly Ala Ala
 39 35 40 45
 42 Leu Ser Pro Leu Pro Glu Val Pro Pro Trp Thr Gly Glu Val Ser Pro
 43 50 55 60
 46 Ala Gln Arg Asp Gly Gly Ala Leu Gly Arg Gly Pro Trp Asp Ser Ser
 47 65 70 75 80
 50 Asp Arg Ser Ala Leu Leu Lys Ser Lys Leu Arg Ala Leu Leu Thr Ala
 51 85 90 95
 54 Pro Arg Ser Leu Arg Arg Ser Ser Cys Phe Gly Gly Arg Met Asp Arg
 55 100 105 110
 58 Ile Gly Ala Gln Ser Gly Leu Gly Cys Asn Ser Phe Arg Tyr
 59 115 120 125
 62 <210> SEQ ID NO: 2
 63 <211> LENGTH: 28
 64 <212> TYPE: PRT
 65 <213> ORGANISM: Homo sapiens
 67 <400> SEQUENCE: 2
 69 Ser Leu Arg Arg Ser Ser Cys Phe Gly Gly Arg Met Asp Arg Ile Gly
 70 1 5 10 15

Does Not Comply
Corrected Diskette Needed
Cp9-415

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Input Set : A:\50318.011001.ST25.txt

Output Set: N:\CRF4\01092006\J562081.raw

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73 Ala Gln Ser Gly Leu Gly Cys Asn Ser Phe Arg Tyr
74          20          25
77 <210> SEQ ID NO: 3
78 <211> LENGTH: 98
79 <212> TYPE: PRT
80 <213> ORGANISM: Homo sapiens
82 <400> SEQUENCE: 3
84 Asn Pro Met Tyr Asn Ala Val Ser Asn Ala Asp Leu Met Asp Phe Lys
85 1          5          10          15
88 Asn Leu Leu Asp His Leu Glu Glu Lys Met Pro Leu Glu Asp Glu Val
89          20          25          30
92 Val Pro Pro Gln Val Leu Ser Glu Pro Asn Glu Glu Ala Gly Ala Ala
93          35          40          45
96 Leu Ser Pro Leu Pro Glu Val Pro Pro Trp Thr Gly Glu Val Ser Pro
97          50          55          60
100 Ala Gln Arg Asp Gly Gly Ala Leu Gly Arg Gly Pro Trp Asp Ser Ser
101 65          70          75          80
104 Asp Arg Ser Ala Leu Leu Lys Ser Lys Leu Arg Ala Leu Leu Thr Ala
105          85          90          95
108 Pro Arg
112 <210> SEQ ID NO: 4
113 <211> LENGTH: 108
114 <212> TYPE: PRT
115 <213> ORGANISM: Homo sapiens
117 <400> SEQUENCE: 4
119 His Pro Leu Gly Ser Pro Gly Ser Ala Ser Asp Leu Glu Thr Ser Gly
120 1          5          10          15
123 Leu Gln Glu Gln Arg Asn His Leu Gln Gly Lys Leu Ser Glu Leu Gln
124          20          25          30
127 Val Glu Gln Thr Ser Leu Glu Pro Leu Gln Glu Ser Pro Arg Pro Thr
128          35          40          45
131 Gly Val Trp Lys Ser Arg Glu Val Ala Thr Glu Gly Ile Arg Gly His
132          50          55          60
135 Arg Lys Met Val Leu Tyr Thr Leu Arg Ala Pro Arg Ser Pro Lys Met
136 65          70          75          80
139 Val Gln Gly Ser Gly Cys Phe Gly Arg Lys Met Asp Arg Ile Ser Ser
140          85          90          95
143 Ser Ser Gly Leu Gly Cys Lys Val Leu Arg Arg His
144          100          105
147 <210> SEQ ID NO: 5
148 <211> LENGTH: 32
149 <212> TYPE: PRT
150 <213> ORGANISM: Homo sapiens
152 <400> SEQUENCE: 5
154 Ser Pro Lys Met Val Gln Gly Ser Gly Cys Phe Gly Arg Lys Met Asp
155 1          5          10          15
158 Arg Ile Ser Ser Ser Ser Gly Leu Gly Cys Lys Val Leu Arg Arg His
159          20          25          30
162 <210> SEQ ID NO: 6

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RAW SEQUENCE LISTING

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Input Set : A:\50318.011001.ST25.txt

Output Set: N:\CRF4\01092006\J562081.raw

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163 <211> LENGTH: 76
164 <212> TYPE: PRT
165 <213> ORGANISM: Homo sapiens
167 <400> SEQUENCE: 6
169 His Pro Leu Gly Ser Pro Gly Ser Ala Ser Asp Leu Glu Thr Ser Gly
170 1 5 10 15
173 Leu Gln Glu Gln Arg Asn His Leu Gln Gly Lys Leu Ser Glu Leu Gln
174 20 25 30
177 Val Glu Gln Thr Ser Leu Glu Pro Leu Gln Glu Ser Pro Arg Pro Thr
178 35 40 45
181 Gly Val Trp Lys Ser Arg Glu Val Ala Thr Glu Gly Ile Arg Gly His
182 50 55 60
185 Arg Lys Met Val Leu Tyr Thr Leu Arg Ala Pro Arg
186 65 70 75
189 <210> SEQ ID NO: 7
190 <211> LENGTH: 378
191 <212> TYPE: DNA
192 <213> ORGANISM: Homo sapiens
194 <400> SEQUENCE: 7
195 aatcccatgt acaatgccgt gtccaacgca gacctgatgg atttcaagaa tttgctggac 60
197 catttggaag aaaagatgcc tttagaagat gaggtcgtgc cccacaagt gctcagtga 120
199 ccgaatgaag aagcgggggc tgctctcagc cccctccctg aggtgcctcc ctggaccggg 180
201 gaagtcagcc cagcccagag agatggaggt gccctcgggc ggggccctg ggactcctct 240
203 gatcgatctg ccttcctaaa aagcaagctg agggcgctgc tactgcccc tcggagcctg 300
205 cggagatcca gctgcttcgg gggcaggatg gacaggattg gagcccagag cggactgggc 360
207 tgtaacagct tccggtac 378
210 <210> SEQ ID NO: 8
211 <211> LENGTH: 84
212 <212> TYPE: DNA
213 <213> ORGANISM: Homo sapiens
215 <400> SEQUENCE: 8
216 agcctgcgga gatccagctg cttcgggggc aggatggaca ggattggagc ccagagcgga 60
218 ctgggctgta acagcttccg gtac 84
221 <210> SEQ ID NO: 9
222 <211> LENGTH: 294
223 <212> TYPE: DNA
224 <213> ORGANISM: Homo sapiens
226 <400> SEQUENCE: 9
227 aatcccatgt acaatgccgt gtccaacgca gacctgatgg atttcaagaa tttgctggac 60
229 catttggaag aaaagatgcc tttagaagat gaggtcgtgc cccacaagt gctcagtga 120
231 ccgaatgaag aagcgggggc tgctctcagc cccctccctg aggtgcctcc ctggaccggg 180
233 gaagtcagcc cagcccagag agatggaggt gccctcgggc ggggccctg ggactcctct 240
235 gatcgatctg ccttcctaaa aagcaagctg agggcgctgc tactgcccc tcgg 294
238 <210> SEQ ID NO: 10
239 <211> LENGTH: 324
240 <212> TYPE: DNA
241 <213> ORGANISM: Homo sapiens
243 <400> SEQUENCE: 10
244 caccgcgtgg gcagccccgg ttcagcctcg gacttggaaa cgtccgggtt acaggagcag 60

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246 cgcaaccatt tgcagggcaa actgtcggag ctgcaggtgg agcagacatc cctggagccc 120
 248 ctccaggaga gccccgtcc cacaggtgtc tggaagtccc gggaggtagc caccgagggc 180
 250 atccgtgggc accgcaaaat ggtcctctac accctgcggg caccacgaag cccaagatg 240
 252 gtgcaagggt ctggctgctt tgggaggaag atggaccgga tcagctcctc cagtggcctg 300
 254 ggctgcaaag tgctgaggcg gcat 324
 257 <210> SEQ ID NO: 11
 258 <211> LENGTH: 96
 259 <212> TYPE: DNA
 260 <213> ORGANISM: Homo sapiens
 262 <400> SEQUENCE: 11
 263 agcccaaga tgggtgcaagg gtctggctgc tttgggagga agatggaccg gatcagctcc 60
 265 tccagtggcc tgggctgcaa agtgctgagg cggcat 96
 268 <210> SEQ ID NO: 12
 269 <211> LENGTH: 228
 270 <212> TYPE: DNA
 271 <213> ORGANISM: Homo sapiens
 273 <400> SEQUENCE: 12
 274 caccgctgg gcagccccgg ttcagcctcg gacttggaaa cgtccgggtt acaggagcag 60
 276 cgcaaccatt tgcagggcaa actgtcggag ctgcaggtgg agcagacatc cctggagccc 120
 278 ctccaggaga gccccgtcc cacaggtgtc tggaagtccc gggaggtagc caccgagggc 180
 280 atccgtgggc accgcaaaat ggtcctctac accctgcggg caccacga 228
 283 <210> SEQ ID NO: 13
 284 <211> LENGTH: 25
 285 <212> TYPE: PRT
 286 <213> ORGANISM: Artificial sequence
 288 <220> FEATURE:
 289 <223> OTHER INFORMATION: *if 2137 is Artificial, explanation they should be an explanation to what is the source?*
 W--> 291 <400> 13
 293 Ser Gly Leu Gln Glu Gln Arg Asn His Leu Arg Ser Ala Leu Leu Lys
 294 1 5 10 15
 297 Ser Lys Leu Arg Ala Leu Leu Thr Ala
 298 20 25
 301 <210> SEQ ID NO: 14
 302 <211> LENGTH: 107
 303 <212> TYPE: PRT
 304 <213> ORGANISM: Artificial sequence
 306 <220> FEATURE:
 307 <223> OTHER INFORMATION: *Same Error*
 W--> 309 <400> 14
 311 His Pro Leu Gly Ser Pro Gly Ser Ala Ser Asp Leu Glu Thr Ser Gly
 312 1 5 10 15
 315 Leu Gln Glu Gln Arg Asn His Leu Gln Gly Lys Leu Ser Glu Leu Gln
 316 20 25 30
 319 Val Glu Gln Thr Ser Glu Asp Glu Val Val Pro Pro Gln Val Leu Ser
 320 35 40 45
 323 Glu Pro Asn Glu Glu Ala Gly Ala Ala Leu Ser Pro Leu Pro Glu Val
 324 50 55 60
 327 Pro Pro Trp Thr Gly Glu Val Ser Pro Ala Gln Arg Asp Gly Gly Ala
 328 65 70 75 80

is Artificial, explanation they should be an explanation to what is the source?
 Pls see Item # 11 on Error Summary Sheet.

RAW SEQUENCE LISTING

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Input Set : A:\50318.011001.ST25.txt

Output Set: N:\CRF4\01092006\J562081.raw

331 Leu Gly Arg Gly Pro Trp Asp Ser Ser Asp Arg Ser Ala Leu Leu Lys
 332 85 90 95
 335 Ser Lys Leu Arg Ala Leu Leu Thr Ala Pro Arg
 336 100 105
 339 <210> SEQ ID NO: 15
 340 <211> LENGTH: 81
 341 <212> TYPE: PRT
 342 <213> ORGANISM: Artificial sequence
 344 <220> FEATURE:
 345 <223> OTHER INFORMATION:
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 349 Ser Asp Leu Glu Thr Ser Gly Leu Gln Glu Gln Arg Asn His Leu Gln
 350 1 5 10 15
 353 Gly Lys Leu Ser Asp His Leu Glu Glu Lys Met Pro Leu Glu Asp Glu
 354 20 25 30
 357 Val Val Pro Pro Gln Val Leu Ser Glu Pro Asn Glu Glu Ala Gly Ala
 358 35 40 45
 361 Ala Leu Ser Pro Leu Pro Glu Val Pro Pro Trp Thr Gly Glu Val Ser
 362 50 55 60
 365 Pro Ala Gln Arg Asp Gly Gly Ala Leu Gly Arg Gly Pro Trp Asp Ser
 366 65 70 75 80
 369 Ser
 373 <210> SEQ ID NO: 16
 374 <211> LENGTH: 4
 375 <212> TYPE: PRT
 376 <213> ORGANISM: Artificial sequence
 378 <220> FEATURE:
 379 <223> OTHER INFORMATION:
 W--> 381 <400> 16
 383 Gly Lys Tyr Gly
 384 1
 387 <210> SEQ ID NO: 17
 388 <211> LENGTH: 174
 389 <212> TYPE: PRT
 390 <213> ORGANISM: Artificial sequence
 392 <220> FEATURE:
 393 <223> OTHER INFORMATION:
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 397 His Pro Leu Gly Ser Pro Gly Ser Ala Ser Asp Leu Glu Thr Ser Gly
 398 1 5 10 15
 401 Leu Gln Glu Gln Arg Asn His Leu Gln Gly Lys Leu Ser Glu Leu Gln
 402 20 25 30
 405 Val Glu Gln Thr Ser Leu Glu Pro Leu Gln Glu Ser Pro Arg Pro Thr
 406 35 40 45
 409 Gly Val Trp Lys Ser Arg Glu Val Ala Thr Glu Gly Ile Arg Gly His
 410 50 55 60
 413 Arg Lys Met Val Leu Tyr Thr Leu Arg Ala Pro Arg Asn Pro Met Tyr
 414 65 70 75 80
 417 Asn Ala Val Ser Asn Ala Asp Leu Met Asp Phe Lys Asn Leu Leu Asp

*Same Error. Pls Explain
 the Source
 of Genetic
 Material;*

Same

VERIFICATION SUMMARY

DATE: 01/09/2006

PATENT APPLICATION: US/10/562,081

TIME: 11:14:16

Input Set : A:\50318.011001.ST25.txt

Output Set: N:\CRF4\01092006\J562081.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:291 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:289
L:309 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:307
L:347 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:345
L:381 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:379
L:395 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:17,Line#:393
L:449 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:18,Line#:447
L:471 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:19,Line#:469
L:541 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:20,Line#:539
L:559 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:21,Line#:557
L:573 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:22,Line#:571
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L:755 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:32,Line#:753